CLAIMS:

- 1. An allelic ladder mixture comprising one or more of the following allelic ladders :-
- i) an allelic ladder for locus HUMVWFA31/A comprising one or more of alleles comprising or consisting of sequences :-

TCTA TCTG TCTA (TCTG) 4 (TCTA);

TCTA (TCTG) $_4$ (TCTA) $_7$; or

 $(\text{TCTA})_2$ $(\text{TCTG})_4$ $(\text{TCTA})_3$ TCCA $(\text{TCTA})_3$ or at least 75% homologous thereto;

- ii) an allelic ladder for locus HUMTHO1 comprising or consisting of sequence :-
- $(\text{TCAT})_4$ CAT $(\text{TCAT})_7$ TCGT TCAT; or at least 75% homologous thereto;
- iii) an allelic ladder for locus D8S1179 comprising one or more of alleles :-

(TCTA) a;

(TCTA)₂ TCTG(TCTA)₁₆ or at least 75% homologous thereto;

iv) an allelic ladder for locus HUMFIBRA/FGA comprising
one or more of alleles comprising or consisting of the
sequences :-

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂;

 $\left(\text{TTTC}\right)_3 \ \text{TTTT} \ \text{TTCT} \ \left(\text{CTTT}\right)_{13} \ \text{CCTT} \ \left(\text{CTTT}\right)_5 \ \text{CTCC} \ \left(\text{TTCC}\right)_2;$

 ${\rm (TTTC)_{\,_3}\ TTTT\ TTCT\ (CTTT)_{\,_{16}}\ CCTT\ (CTTT)_{\,_5}\ CTCC\ (TTCC)_{\,_2};}$

 $(TTTC)_4$ TTTT TT $(CTTT)_{15}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$;

 $(TTTC)_4$ TTTT TT $(CTTT)_{16}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$;

 $\left(\text{TTTC} \right)_4 \ \text{TTTT} \ \text{TT} \ \left(\text{CTTT} \right)_{17} \ \left(\text{CTTC} \right)_3 \ \left(\text{CTTT} \right)_3 \ \text{CTCC} \ \left(\text{TTCC} \right)_4;$

(TTTC) $_4$ TTTT TT (CTTT) $_8$ (CTGT) $_4$ (CTTT) $_{13}$ (CTTC) $_4$ (CTTT) $_3$

CTCC (TTCC)₄;

 $(\mathrm{TTTC})_4$ TTTT TT $(\mathrm{CTTT})_8$ $(\mathrm{CTGT})_5$ $(\mathrm{CTTT})_{13}$ $(\mathrm{CTTC})_4$ $(\mathrm{CTTT})_3$

CTCC (TTCC)₄;

 $(TTTC)_4 \ TTTT \ TT \ (CTTT)_{11} \ (CTGT)_3 \ (CTTT)_{14} \ (CTTC)_3 \ (CTTT)_3$ CTCC $(TTCC)_4;$

- (TTTC) $_4$ TTTT TT (CTTT) $_{14}$ (CTGT) $_3$ (CTTT) $_{14}$ (CTTC) $_4$ (CTTT) $_3$ CTCC (TTCC) $_4$; or at least 75% homologous thereto;
- v) an allelic ladder for locus D21S11 comprising one or more of alleles comprising or consisting of sequences :-
- (TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA(TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_6$ TCGTCT;
 - (TCTA) $_{\text{5}}$ (TCTG) $_{\text{6}}$ (TCTA) $_{\text{3}}$ TCA (TCTA) $_{\text{2}}$ TCCATA (TCTA) $_{\text{9}}$ TCGTCT;
 - $(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{10}$ TCGTCT;
- (TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_8$ TCGTCT;
- (TCTA) $_5$ (TCTG) $_5$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_6$ TCGTCT;
- (TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{10}$ TCGTCT;
- (TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{11}$ TCGTCT;
- (TCTA) $_{6}$ (TCTG) $_{5}$ (TCTA) $_{3}$ TA (TCTA) $_{3}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{11}$ TCGTCT;
- (TCTA) $_5$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_1$ 2 TCGTCT;
- (TCTA) $_5$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{12}$ TA TCTA TCGTCT;
- (TCTA), (TCTG), (TCTA), TA (TCTA), TCA (TCTA), TCCATA (TCTA), TA TCTA TCGTCT;
- (TCTA) $_{\rm 5}$ (TCTG) $_{\rm 6}$ (TCTA) $_{\rm 3}$ TA (TCTA) $_{\rm 3}$ TCA (TCTA) $_{\rm 2}$ TCCATA (TCTA) $_{\rm 14}$ TATCTA TCGTCT;
- (TCTA) $_{10}$ (TCTG) $_{5}$ (TCTA) $_{3}$ TA (TCTA) $_{3}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{12}$ TCGTCT;
- ${\rm (TCTA)_{11}} \ \ {\rm (TCTG)_5} \ \ {\rm (TCTA)_3} \ \ {\rm TA} \ \ {\rm (TCTA)_3} \ \ {\rm TCA} \ \ {\rm (TCTA)_2} \ \ {\rm TCCATA}$

(TCTA) $_{11}$ (TCTG) $_{5}$ (TCTA) $_{3}$ TA (TCTA) $_{3}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{13}$ TCGTCT; or

 ${\rm (TCTA)_{13}} \ {\rm (TCTG)_5} \ {\rm (TCTA)_3} \ {\rm TA} \ {\rm (TCTA)_3} \ {\rm TCA} \ {\rm (TCTA)_2} \ {\rm TCCATA}$ ${\rm (TCTA)_{12}} \ {\rm TCGTCT}; \ {\rm or \ at \ least} \ 75\% \ {\rm homologous} \ {\rm thereto};$

vi) an allelic ladder for locus D18S51 comprising an allele comprising or consisting of sequence :-

(AGAA); or at least 75% homologous thereto.

- 2. An allelic ladder mixture according to claim 1 in which the mixture includes allelic ladders for a plurality of loci selected from HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 and D18S51.
- 3. An allelic ladder mixture according to claim 1 the mixture including allelic ladders for at least four loci.
- 4. An allelic ladder mixture according to claim 1 in which the mixture includes an amelogenin sex test.
- 5. An allelic ladder mixture according to claim 1 in which the allelic ladders in the mixture includes at least 7 alleles.
- 6. An allelic ladder mixture according to claim 1 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 9 alleles; the HUMTHO1 allelic ladder includes at least 7; the D8S1179 allelic ladder includes at least 9 alleles; the HUMFIBRA/FGA allelic ladder includes at least 18 alleles or is present as HUMFIBRA/FGA/LW and HUMFIBRA/FGA/HW with the HUMFIBRA/FGA/LW ladder including at least 16 alleles, the HUMFIBRA/FGA/HW ladder including at least 6 alleles; the D21S11 allelic ladder includes at least 14 alleles; and the D18S51 ladder includes at least 15 alleles.

- 7. An allelic ladder mixture according to claim 1 in which one or more of the allelic ladders in the mixture comprises at least 4 pairs of alleles 4 base pairs from each other.
- 8. An allelic ladder mixture according to claim 1 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 7 pairs of alleles 4 base pairs from each other; the HUMTHO1 allelic ladder includes at least 5 pairs of alleles 4 base pairs from each other; the D8S1179 allelic ladder includes at least 8 pairs of alleles 4 base pairs from each other; the HUMFIBRA/FGA allelic ladder includes at least 17 pairs of alleles 4 base pairs from each other; the D21S11 allelic ladder includes at least 3 pairs of alleles 4 base pairs from each other; and the D18S51 ladder includes at least 13 pairs of alleles 4 base pairs from each other.
- 9. An allelic ladder mixture according to claim 8 in which the D21S11 allelic ladder includes at least 8 pairs of alleles 8 base pairs from each other.
- 10. An allelic ladder mixture according to claim 1 in which the ladders, if present, are provided such that the HUMVWFA31/A ladder includes alleles ranging from 130 base pairs upwards and/or from 166 base pairs downwards; the HUMTHO1 ladder includes alleles ranging from 150 base pairs upwards and/or 189 base pairs downwards; the D8S1179 ladder includes alleles ranging from 157 base pairs upwards and/or 201 base pairs downwards; the HUMFIBRA/FGA ladder includes alleles ranging from 173 base pairs upwards and/or 298 base pairs downwards; the D21S11 ladder includes alleles ranging from 203 base pairs upwards and/or 255 base pairs downwards; and the D18S51 ladder includes alleles ranging from 270 base pairs upwards and/or 326 downwards.
- 11. An allelic ladder mixture comprising an allelic ladder for one or more of the following loci, with lowest molecular

weight allele and/or uppermost molecular weight allele as
follows :-

- 12. An allelic ladder mixture according to claim 11 in which the loci ladders have both the upper and lower limits specified.
- 13. An allelic ladder mixture according to claim 11 in which the mixture includes allelic ladders for loci HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 and D18S51.
- 14. A method of analysing one or more samples comprising :
 - a) obtaining genomic DNA from the sample;
 - b) amplifying the DNA;
- c) obtaining an indication of one or more of the constituent parts of the sample; and comparing the indications with an allelic ladder mixture comprising one or more of the following allelic ladders:-
- i) an allelic ladder for locus HUMVWFA31/A comprising one or more of alleles comprising or consisting of sequences :- TCTA TCTG TCTA (TCTG) $_4$ (TCTA) $_3$;

TCTA (TCTG) $_4$ (TCTA) $_7$; or (TCTA) $_2$ (TCTG) $_4$ (TCTA) $_3$ TCCA (TCTA) $_3$

ii) an allelic ladder for locus HUMTHO1 comprising or consisting of sequence :-

(TCAT), CAT (TCAT), TCGT TCAT;

iii) an allelic ladder for locus D8S1179 comprising one or more of alleles comprising or consisting of sequences :- (TCTA)8; or

(TCTA)₂ TCTG (TCTA)₁₆;

iv) an allelic ladder for locus HUMFIBRA/FGA comprising one or more of alleles comprising or consisting of the sequences :-

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂; (TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₇; (TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₃; (TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄; (TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄; (TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄; (TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₄ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄; (TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄; $(TTTC)_4$ TTT TT $(CTTT)_{11}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC (TTCC)₄; $(TTTC)_4$ TTT TT $(CTTT)_{10}$ $(CTGT)_5$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC (TTCC)₄; (TTTC)₄ TTTT TT (CTTT)₁₂ (CTGT)₅ (CTTT)₁₄ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄; or $(TTTC)_4$ TTTT TT $(CTTT)_{14}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_4$ $(CTTT)_3$ CTCC (TTCC)₄;

(TCTA) $_5$ (TCTG) $_5$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_9$ TCGTCT;

(TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_2$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{10}$ TCGTCT;

(TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{11}$ TCGTCT;

(TCTA) $_{6}$ (TCTG) $_{5}$ (TCTA) $_{3}$ TA (TCTA) $_{3}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{11}$ TCGTCT;

(TCTA) $_5$ (TCTG) $_6$ (TCTA) $_7$ TA (TCTA) $_7$ TCA (TCTA) $_2$ TCCATA (TCTA) $_1$, TCGTCT;

(TCTA) $_5$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{11}$ TA TCTA TCGTCT;

(TCTA) $_{5}$ (TCTG) $_{6}$ (TCTA) $_{3}$ TA (TCTA) $_{7}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{12}$ TA TCTA TCGTCT;

(TCTA) $_{5}$ (TCTG) $_{6}$ (TCTA) $_{3}$ TA (TCTA) $_{2}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{13}$ TA TCTA TCGTCT;

(TCTA) $_5$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{14}$ TATCTA TCGTCT;

(TCTA) $_{\rm 10}$ (TCTG) $_{\rm S}$ (TCTA) $_{\rm 3}$ TA (TCTA) $_{\rm 3}$ TCA (TCTA) $_{\rm 7}$ TCCATA (TCTA) $_{\rm 12}$ TCGTCT;

(TCTA) $_{\rm 11}$ (TCTG) $_{\rm 5}$ (TCTA) $_{\rm 3}$ TA (TCTA) $_{\rm 2}$ TCA (TCTA) $_{\rm 2}$ TCCATA (TCTA) $_{\rm 12}$ TCGTCT;

(TCTA) $_{\rm 11}$ (TCTG) $_{\rm 5}$ (TCTA) $_{\rm 3}$ TA (TCTA) $_{\rm 3}$ TCA (TCTA) $_{\rm 2}$ TCCATA (TCTA) $_{\rm 13}$ TCGTCT; or

(TCTA) $_{\mbox{\tiny 13}}$ (TCTG) $_{\mbox{\tiny 5}}$ (TCTA) $_{\mbox{\tiny 3}}$ TA (TCTA) $_{\mbox{\tiny 3}}$ TCA (TCTA) $_{\mbox{\tiny 2}}$ TCCATA (TCTA) $_{\mbox{\tiny 12}}$

vi) an allelic ladder for locus D18S51 comprising an allele comprising or consisting of sequence :
(AGAA);

including allelic ladders or alleles 75% homologous thereto.

15. A method according to claim 14 in which the DNA sample is one or more of a sample taken from the scene of a crime, a sample associated with the scene of a crime, a sample obtained from a suspect, a sample obtained from a human under consideration (for instance for paternity or maternity analysis) or a reference sample.

(TCTA), TCGTCT;

- 16. A method according to claim 14 in which the sample is amplified using a polymerase chain reaction and primers for one or more of loci HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 or D18S51 are employed.
- One or more alleles comprising or consisting of sequences 17. TCTA TCTG TCTA (TCTG), (TCTA); TCTA (TCTG)₄ (TCTA)₇; (TCTA)₂ (TCTG)₄ (TCTA)₃ TCCA (TCTA)₃; (TCAT), CAT (TCAT), TCGT TCAT; (TCTA),; (TCTA)₂ TCTG (TCTA)₁₆; (TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂; (TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₂; (TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₃; (TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄; $(TTTC)_4$ TTTT TT $(CTTT)_{16}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$; (TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC), (CTTT)₃ CTCC (TTCC)₄; $(TTTC)_4$ TTTT TT $(CTTT)_8$ $(CTGT)_4$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC (TTCC)₄; (TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₅ CTCC (TTCC)₄; $(TTTC)_4$ TTTT TT $(CTTT)_{11}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC (TTCC)₄; (TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄; $(TTTC)_4$ TTTT TT $(CTTT)_{12}$ $(CTGT)_5$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC (TTCC)₄; $(TTTC)_4$ TTTT TT $(CTTT)_{14}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_4$ $(CTTT)_3$ CTCC (TTCC) 4; (TCTA)₄ (TCTG)₆ (TCTA)₃ TA(TCTA)₃ TCA (TCTA)₂ (TCTA) 6 TCGTCT; (TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₃ TCGTCT; (TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀ TCGTCT; (TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA

- (TCTA) $_5$ (TCTG) $_5$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_9$ TCGTCT;
- (TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{10}$ TCGTCT;
- (TCTA) $_4$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{11}$ TCGTCT;
- (TCTA) $_{6}$ (TCTG) $_{5}$ (TCTA) $_{3}$ TA (TCTA) $_{3}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{11}$ TCGTCT;
- (TCTA) $_{\rm S}$ (TCTG) $_{\rm G}$ (TCTA) $_{\rm 3}$ TA (TCTA) $_{\rm 3}$ TCA (TCTA) $_{\rm 2}$ TCCATA (TCTA) $_{\rm 12}$ TCGTCT;
- (TCTA) $_{\rm 5}$ (TCTG) $_{\rm 6}$ (TCTA) $_{\rm 2}$ TA (TCTA) $_{\rm 3}$ TCA (TCTA) $_{\rm 2}$ TCCATA (TCTA) $_{\rm 11}$ TA TCTA TCGTCT;
- (TCTA) $_{5}$ (TCTG) $_{6}$ (TCTA) $_{3}$ TA (TCTA) $_{3}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{12}$ TA TCTA TCGTCT;
- (TCTA) $_{5}$ (TCTG) $_{6}$ (TCTA) $_{3}$ TA (TCTA) $_{3}$ TCA (TCTA) $_{2}$ TCCATA (TCTA) $_{13}$ TA TCTA TCGTCT;
- (TCTA) $_5$ (TCTG) $_6$ (TCTA) $_3$ TA (TCTA) $_3$ TCA (TCTA) $_2$ TCCATA (TCTA) $_{14}$ TATCTA TCGTCT;
- (TCTA) $_{\rm 10}$ (TCTG) $_{\rm 5}$ (TCTA) $_{\rm 3}$ TA (TCTA) $_{\rm 3}$ TCA (TCTA) $_{\rm 2}$ TCCATA (TCTA) $_{\rm 12}$ TCGTCT;
- ${\rm (TCTA)_{11}} \ {\rm (TCTG)_5} \ {\rm (TCTA)_3} \ {\rm TA} \ {\rm (TCTA)_3} \ {\rm TCA} \ {\rm (TCTA)_2} \ {\rm TCCATA}$
- (TCTA) $_{\rm 11}$ (TCTG) $_{\rm 5}$ (TCTA) $_{\rm 3}$ TA (TCTA) $_{\rm 3}$ TCA (TCTA) $_{\rm 2}$ TCCATA (TCTA) $_{\rm 13}$ TCGTCT;
- (TCTA) $_{\mbox{\tiny 1,3}}$ (TCTG) $_{\mbox{\tiny 5}}$ (TCTA) $_{\mbox{\tiny 3}}$ TA (TCTA) $_{\mbox{\tiny 3}}$ TCA (TCTA) $_{\mbox{\tiny 2}}$ TCCATA (TCTA) $_{\mbox{\tiny 12}}$
 - (AGAA) ; or at least 75% homologous thereto.
- 18. One or more alleles according to claim 16 in which the alleles are provided purified from alleles other than those of HUMVWFA31/A, HUMTH01, D8S1179, HUMFIBRA/FGA, D21511, D18551 or AMG loci.
- 19. The use of an allelic ladder according to claim 1 for comparison with a DNA analysis result.

- 20. The use of claim 19 wherein the analysis is a DNA profile of a sample and the profile is based on analysis of one or more of loci HUMVWFA31/A, HUMTH01, D9S1179, HUMFIBRA/FGA, D21S11, D18S51 OR AMG.
- 21. A method of producing an allelic ladder or mixture thereof by subjecting the ladders of any of claim 1 to PCR.
- 22. A method of producing an allelic ladder or mixture thereof by subjecting the alleles of any of claim 17 to PCR.